CLUSTAL W (1.82) Multiple Sequence Alignments

Sequence format is Pearson
Sequence 1: HrpW   424 aa
Sequence 2: HopPtoA_SEQIDNO7   486 aa
Start of Pairwise alignments
Aligning...
Sequences (1:2) Aligned. Score: 6
Guide tree   file created: [/ebi/extserv/old-work/199548.12283.dnd]
Start of Multiple Alignment
There are 1 groups
Aligning...
Group 1:   Delayed
Sequence:2   Score:3175
Alignment Score 3
CLUSTAL-Alignment file created   [/ebi/extserv/old-work/199548.12283.aln]

199548.12283.aln

CLUSTAL W (1.82) multiple sequence alignment

```
HrpW              MSIGITPRPQQTTTPLDFSALSGKSPQPNTFGEQNTQQAIDPSALLFGSDTQKDVNFGTP   60
HopPtoA_SEQIDNO7  MHINRRVQQPPVTATDSFRTASDASLASSSVRSVSSDQQREINAIADYLTDHVFAAHKLP   60
                  * *.    :   .*:. .* : *. *    ..:. . .::*   : .*:      :  . . *


HrpW              DSTVQNPQDASKPNDSQSNIAKLISALIMSLLQMLTNSNKKQDTNQEQPDSQAPFQNNGG  120
HopPtoA_SEQIDNO7  PADSADGQAAVDVHNAQITALIETRASRLHFEGETPATIADTFAKAEKLDRLATTTSGAL  120
                  :    :  * * . .::*  .      *   : :    . :  .  :: *:  *   *.  ...


HrpW              LGTPSADSGGGGTPDATGGGG--------GDTPSATGGGGGDTPTATGGGGSGGGGTPTA  172
HopPtoA_SEQIDNO7  RATPFAMASLLQYMQPAINKGDWLPAPLKPLTPLISGALSGAMDQVGTKMMDRATGDLHY  180
                  .** * :.       :.: . *         ** :*. .*   .      . . *


HrpW              TGGGSGGTPTATGGGEGGVTPQITPQLANP-------NRTSGTGSVSDTAGSTEQAGKIN  225
HopPtoA_SEQIDNO7  LSASPDRLHDAMAASVKRHSPSLARQVLDTGVAVQTYSARNAVRTVLAPALASRPAVQGA  240
                  .....        *  ...    :*.:: *: :.      . ...:*  .* ::. * :


HrpW              VVKDTIKVGAGEVFDGHGATFTADKSMGNGDQG------ENQKPMFELAEG-------AT  272
HopPtoA_SEQIDNO7  VDLGVSMAGGLAANAGFGNRLLSVQSRDHQRGGALVLGLKDKEPKAQLSEENDWLEAYKA  300
                  *   ..  .*. . *.* : : :* .:    *       :::*:* :*:*         :


HrpW              LKNVNLGENEVDG-------IHVKAKNAQEVTIDNVHAQNVGEDLITVKG--EGGAAVTN  323
HopPtoA_SEQIDNO7  IKSASYSGAALNAGKRMAGLPLDMATDAMGAVRSLVSASSLTQNGLALAGGFAGVGKLQE  360
                  :*... .   ::.       *.:*  .. . * *..: :: ::: *   * . .:  :


HrpW              LNIKNSSAKGADDKVVQLN-----------------ANTHLKIDNFKADDFGTMVRTN  364
HopPtoA_SEQIDNO7  MATKNITDPATKAAVSQLTNLAGSAAVFAGWTTAALTTDPAVKKAESFIQDTVKSTASST  420
                  :  ** :  .:.  * **.                   :  * :.* * . : . :.


HrpW              GGKQFDDMSIELNGIEANHGKFALVKSDSDDLKLATGNIAMTDVKHAYDKTQASTQHTEL  424
HopPtoA_SEQIDNO7  TG-YVADQTVKLAKTVKDMGGEAITHTGASLRNTVNNLRQRPAREADIEEGGTAASPSEI  479
                  *  . * :::* :  * : * *:..::. : ...  . :  :: :::. :*:


HrpW              -------
HopPtoA_SEQIDNO7  PFRPMRS  486
```


199548.12283.dnd

(HrpW:0.46698,HopPtoA_SEQIDNO7:0.46698)